Maintenance of gametophytic self-incompatibility system in spatially structured populations

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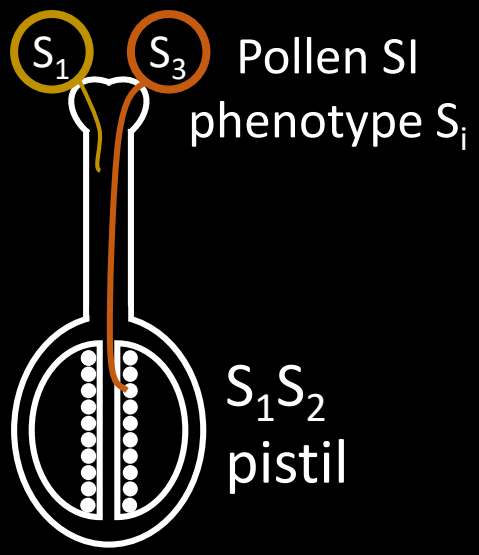
12.01.2018

Self-Incompatibility (SI)



Flowering plants

Self-fertilization avoidance

High diversity

Arabidopsis halleri

Swanson, R., et al. 2004. *Annu. Rev. Genet.* **38**: 793–818.

Self-Incompatibility: multiple independent evolution

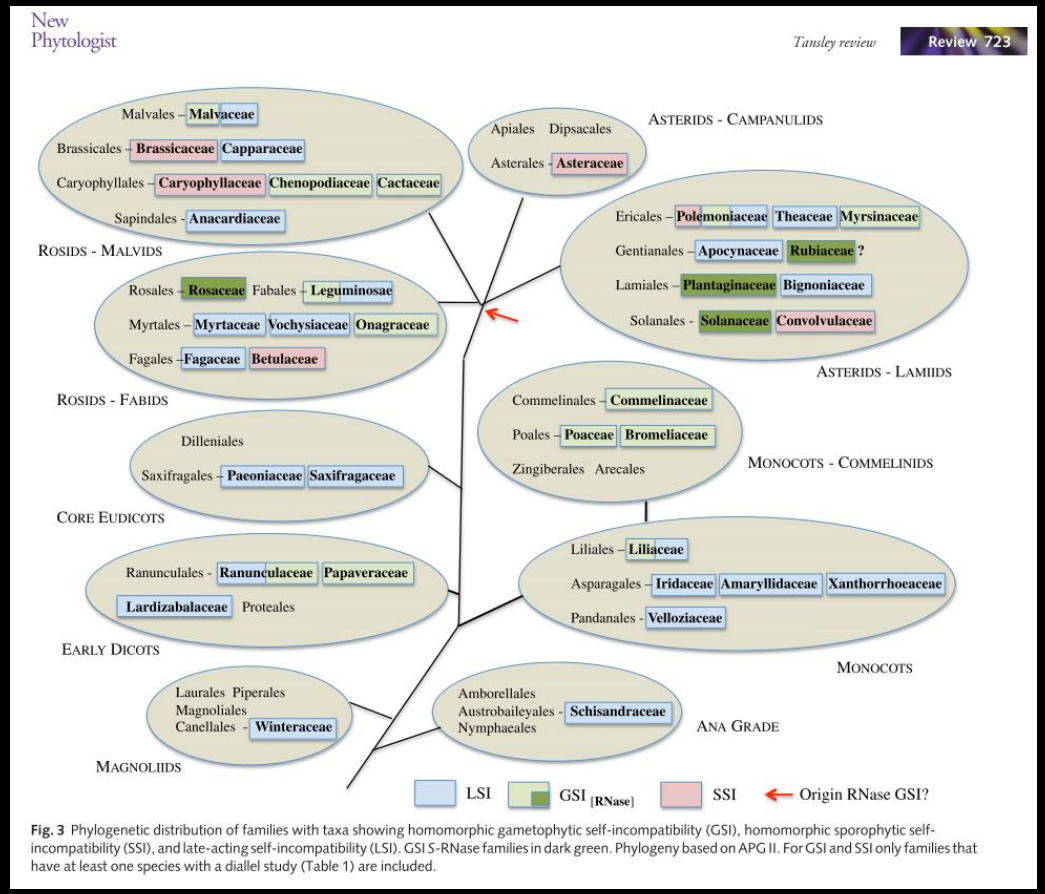
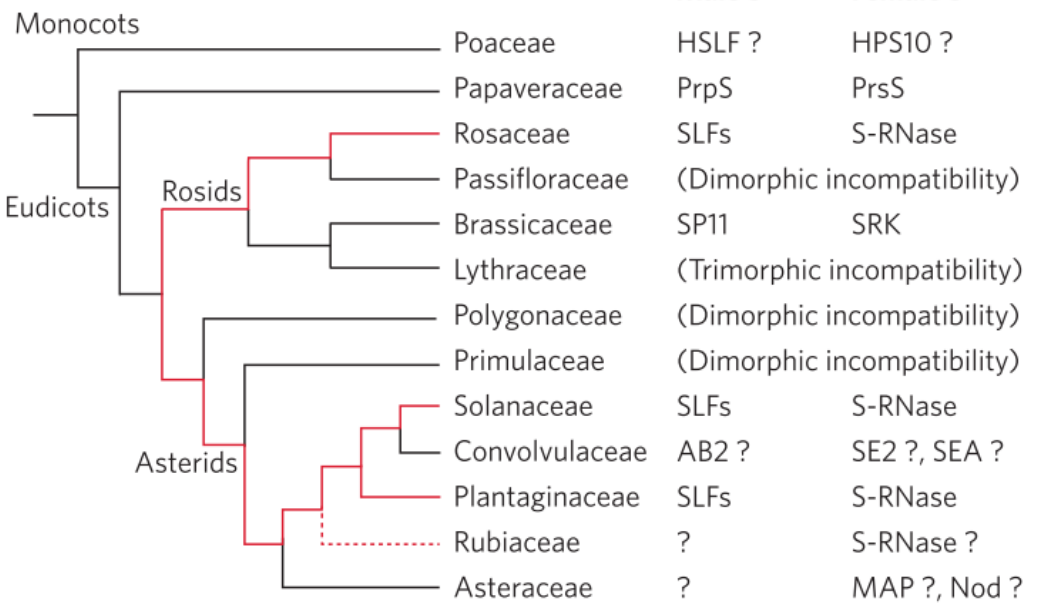


Fig. 3 Phylogenetic distribution of families with taxa showing homomorphic gametophytic self-incompatibility (GSI), homomorphic sporophytic self-incompatibility (SSI), and late-acting self-incompatibility (LSI). GSI *S*-RNase families in dark green. Phylogeny based on APG II. For GSI and SSI only families that have at least one species with a diallel study (Table 1) are included.



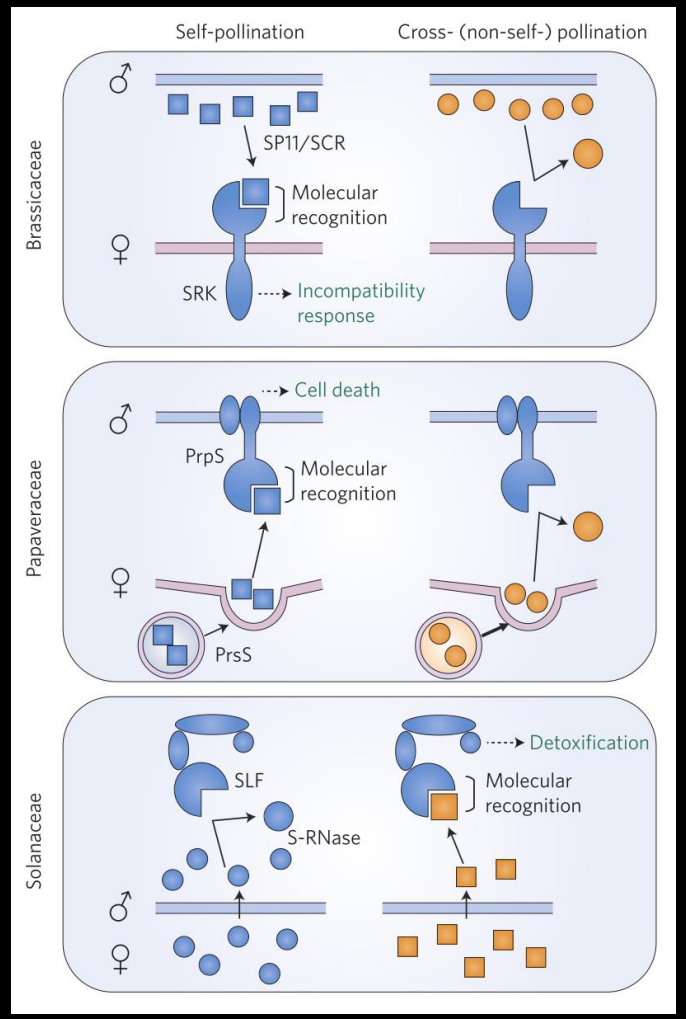
	Male S	Female S
Poaceae	HSLF ?	HPS10 ?
Papaveraceae	PrpS	PrsS
Rosaceae	SLFs	S-RNase
Passifloraceae	(Dimorphic incompatibility)	
Brassicaceae	SP11	SRK
Lythraceae	(Trimorphic incompatibility)	
Polygonaceae	(Dimorphic incompatibility)	
Primulaceae	(Dimorphic incompatibility)	
Solanaceae	SLFs	S-RNase
Convolvulaceae	AB2 ?	SE2 ?, SEA ?
Plantaginaceae	SLFs	S-RNase
Rubiaceae	?	S-RNase ?
Asteraceae	?	MAP ?, Nod ?

Figure 1 | Phylogenic distribution of different SI systems in flowering plants. Families of plants and candidates for the male and female determinants of SI are listed. Red branches indicate the phylogenetic distribution of species adopting S-RNase-based SI.

Gibbs, P.E. 2014. *New Phytol.* **203**: 717–734.

Fujii, S., et al. 2016. *Nat. Plants* **2**: 16130.

Self-Incompatibility: different mechanisms, a single locus

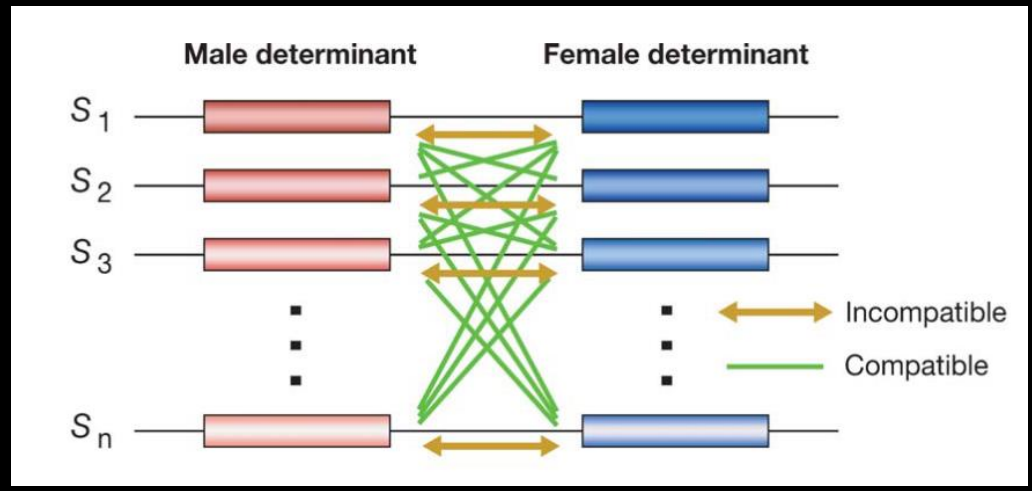


SRK/SCR

PrsS/PrpS

S-Rnase/SLF

S-locus



A single multiallelic locus

Fujii, S., Kubo, K. & Takayama, S. 2016. *Nat. Plants* **2**: 16130. Takayama, S. & Isogai, A. 2005. *Annu. Rev. Plant Biol.* **56**: 467–489.

SI:
a great diversity of allele

TABLE 1. *Number of incompatibility alleles known or estimated to be present in populations, n_p and N_p, and species, n and N, of 19 flowering plants*

System	Species	R	Populations n_p	Populations N_p
Gametophytic one locus	*Nicotiana sanderae*[1]	0·59	15	18
	Oenothera organensis[2]	0·65	28	30
	Trifolium repens[3]	0·07	17	139
		0·19	28	80
		0·28	36	74
		0·22	39	101
	Trifolium pratense[4]	0·16	41	143
		0·09	33	193
	Trifolium hybridum[5]	0·47	12	17
	Papaver rhoeas[6]	0·65	27	35+
		0·68	25	32+
		0·72	31	38+
	Phlox drummondii[7]	0·40	30	45
	Solanum carolinense[8]	0·68	11	12
		0·57	12	14
	Physalis crassifolia[9]	0·39	28	44
	Physalis cinerascens[10]	0·57	12	14
	Lycium andersonii[11]	0·34	22	38
	Witheringia maculata[12]	0·67	10	14
Gametophytic two loci	*Lolium perenne*[13]	0·58	17S	31+*S*
		0·59	17Z	31+*Z*
Sporophytic one locus	*Iberis amara*[14]			>22?
	Raphanus raphanistrum[15]			
	Brassica oleracea[16]			
	Brassica campestris[17]	0·58	16	22
		0·52	18	31
	Sinapis arvensis[18]	0·51	35	43
	Ipomoea trifida[19]	0·96	5	
		0·83	15	
		0·77	19	
		0·83	16	
		0·76	21	
		0·93	6	

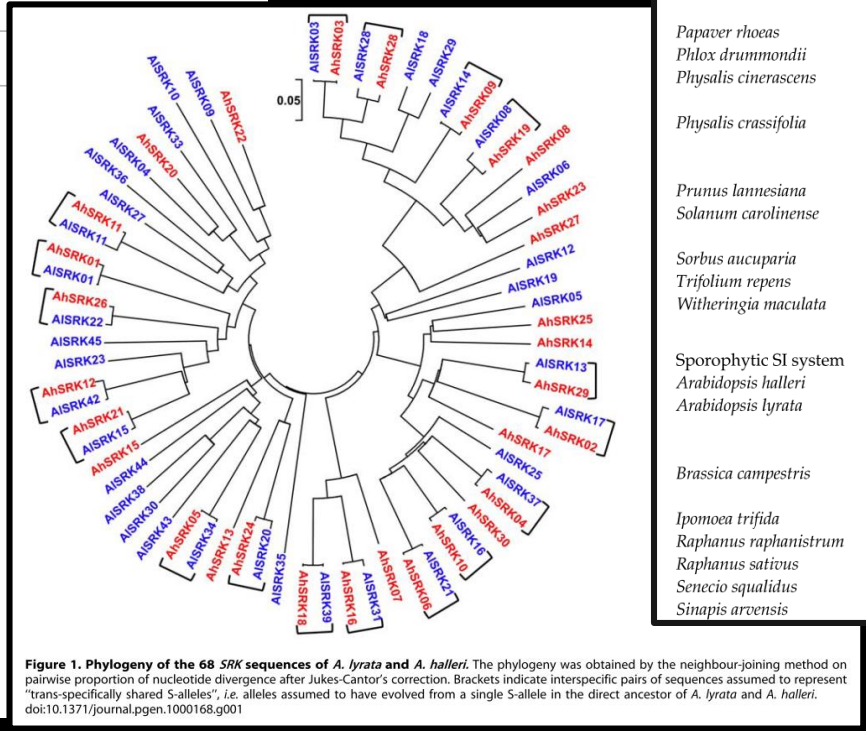


Figure 1. Phylogeny of the 68 *SRK* sequences of *A. lyrata* and *A. halleri*. The phylogeny was obtained by the neighbour-joining method on pairwise proportion of nucleotide divergence after Jukes-Cantor's correction. Brackets indicate interspecific pairs of sequences assumed to represent "trans-specifically shared S-alleles", *i.e.* alleles assumed to have evolved from a single S-allele in the direct ancestor of *A. lyrata* and *A. halleri*.
doi:10.1371/journal.pgen.1000168.g001

Table 1 Summary of empirical studies in natural populations of plants species with gametophytic or sporophytic SI

Species	N_{ind}	$n_{alleles}$	Test of equal allelic frequencies: χ^2 statistic	Significance	Nucleotide polymorphism: π	R_{SD}	References
Gametophytic SI system							
Crataegus monogyna	13	17	11.3	NS*	0.280	4.94†	Raspé & Kohn (2002)
Lycium andersonii	16	22	10.5	NS	0.463	4.74	Richman (2000)
						$P < 0.01$	Raspé & Kohn (2002)
Oenothera organensis	67	34	33.46	NS	—	—	Emerson (1939)
							Campbell & Lawrence (1981)
Papaver rhoeas	51	31	64.26	$P < 0.001$	—	—	Campbell & Lawrence (1981)
Phlox drummondii	24	30		NS	—	—	Levin (1993)
Physalis cinerascens	14	13	14.7	NS	0.208	2.59	Richman & Kohn (1999)
						NS	Richman & Kohn (2000)
Physalis crassifolia	22	28	17.8	NS*	0.387	2.59	Richman *et al.* (1996b)
						NS	Richman (2000)
							Raspé & Kohn (2002)
Prunus lannesiana	67	21	98.8	$P < 0.001$	—	—	Kato & Mukai (2004)
Solanum carolinense	24	12	3.3	NS	—	5.801	Richman *et al.* (1995)
						$P < 0.01$	Richman (2000)
Sorbus aucuparia	20	20	15.8	NS	0.251	7.39	Raspé & Kohn (2002)
Trifolium repens	25	36	13.84‡	NS‡	—	—	Atwood (1944)
Witheringia maculata	12	10	—	—	—	1.48	Richman & Kohn (2000)
						NS	
Sporophytic SI system							
Arabidopsis halleri	20	17	—	—	0.301	8.88	Castric and Vekemans, unpublished
Arabidopsis lyrata	20	11	26.10	$P < 0.001$	0.257	7.59	Mable *et al.* (2003)
							Charlesworth *et al.* (2003)
							Schierup *et al.* (2001b)
Brassica campestris	17	18	28.93‡	$P < 0.05$‡	0.130	8.87	Nou *et al.* (1993)
							Schierup *et al.* (2001b)
Ipomoea trifida	41	16	1144.12‡	$P < 0.0001$‡	—	—	Kowyama *et al.* (1994)
Raphanus raphanistrum	26	13	8.00‡	NS‡	—	—	Sampson (1964, 1967)
Raphanus sativus	29	22	—	—	—	—	Karron *et al.* (1990)
Senecio squalidus	25	6	13.16	$P < 0.05$	—	—	Brennan *et al.* (2003)
Sinapis arvensis	35	35	27.82‡	NS‡	—	—	Stevens & Kay (1989)

Lawrence, M.J. 2000. *Ann. Bot.* **85**: 221–226.

Castric, V., et al. 2008. *PLoS Genet.* **4**.

Castric, V. & Vekemans, X. 2004. *Mol. Ecol.* **13**: 2873–2889.

Self-Compatibility (SC)

Frequent transition SI → SC

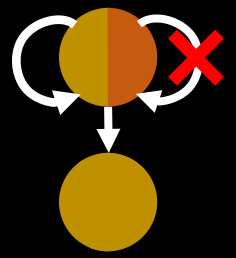
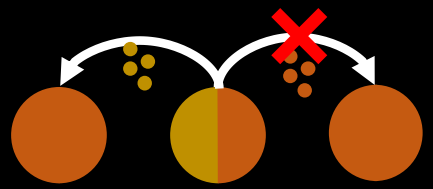
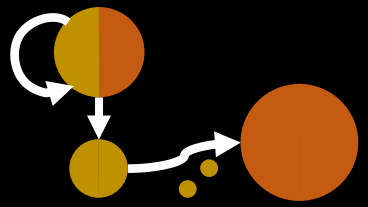
SI and SC in the same specie

Selected when mates are limiting ?

Arabidopsis halleri

Arabidopsis thaliana

SI versus SC

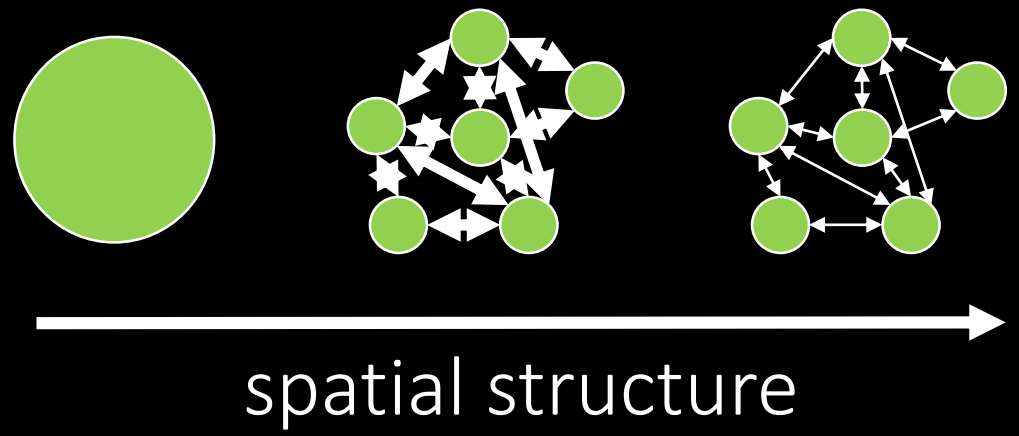
	Self **I**ncompatible	**S**elf **C**ompatible
 Transmission advantage through selfing	✗	✓
 Mate restriction	✓	✗
 Inbreeding depression	✗	✓

Gervais, C., et al. 2014. *Evolution* **68**: 3317–3324.

SI maintenance: spatial structure effect

How spatial structure affects SI system resistance against the invasion by a SC mutant ?

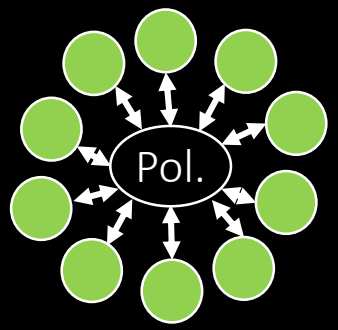
- What is the effect of SI allele number ?
- What is the effect of spatial genetic structure ?



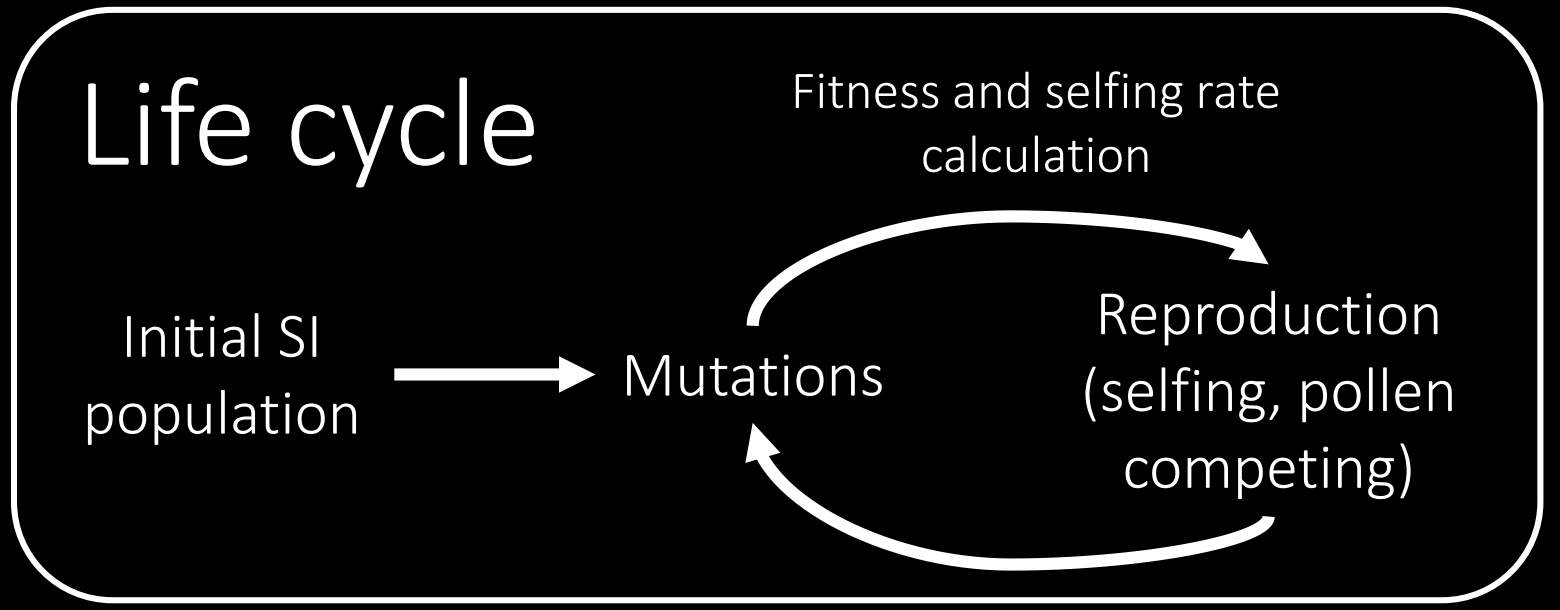
Method: Individual-Based Model

Constant metapopulation size (10*1000 individuals)

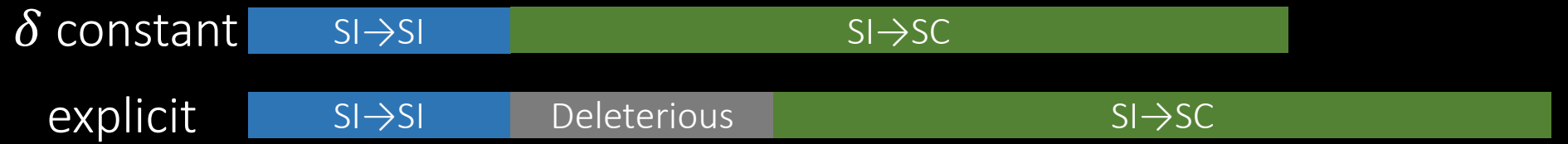
Dispersal through pollen only



Life cycle



Mutations introductions



Method: inbreeding depression modeling

Constant inbreeding depression:

$W_o = 1$

$W_s = 1 - \delta$

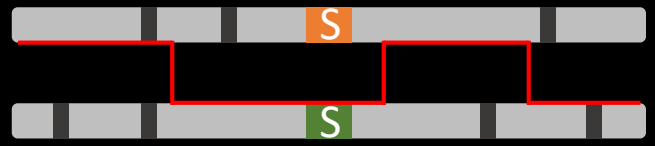
Explicit mutation model: complex inbreeding depression

Infinite number of loci

Deleterious mutations (h, s)

Recombination (L): partially linked to S-locus

$W_i = (1 - sh)^{N_{he}}(1 - s)^{N_{hom}}$



Porcher, E. & Lande, R. 2013. *Evolution* **67**: 3628–3635.

Gervais, C., et al. 2014. *Evolution* **68**: 3317–3324.

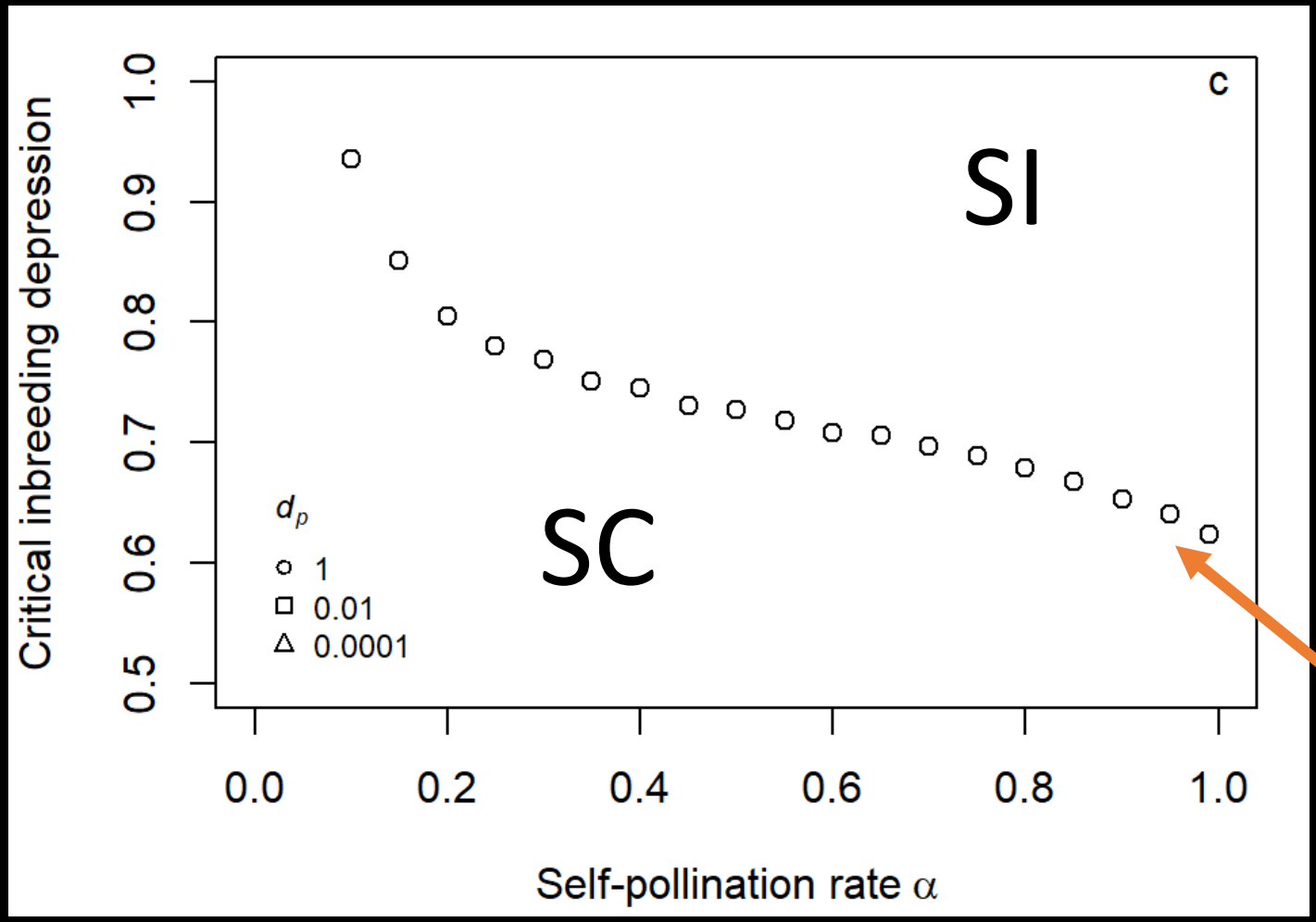
Results

Spatial structure effect: pollen dispersal rate

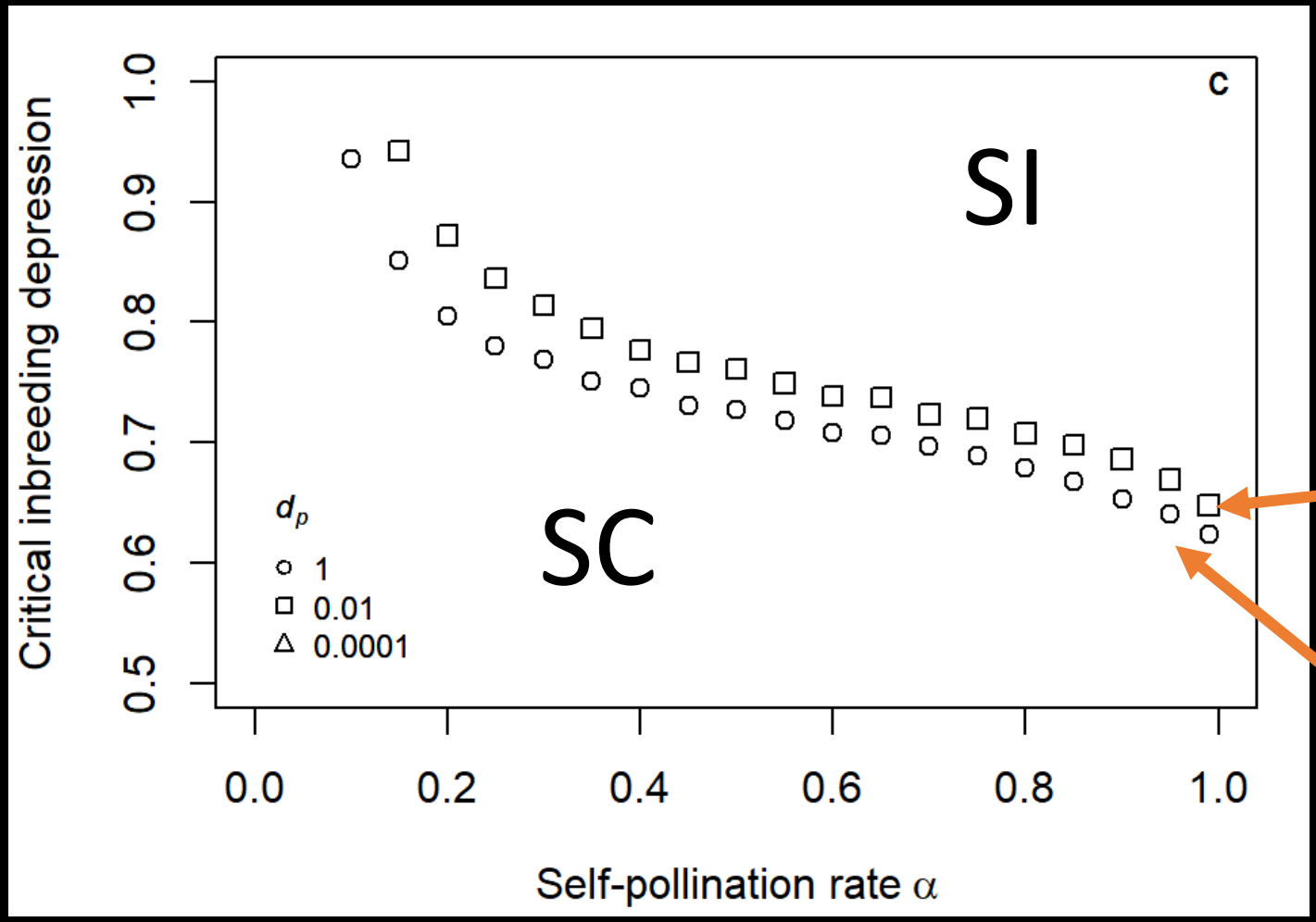
Number of allele

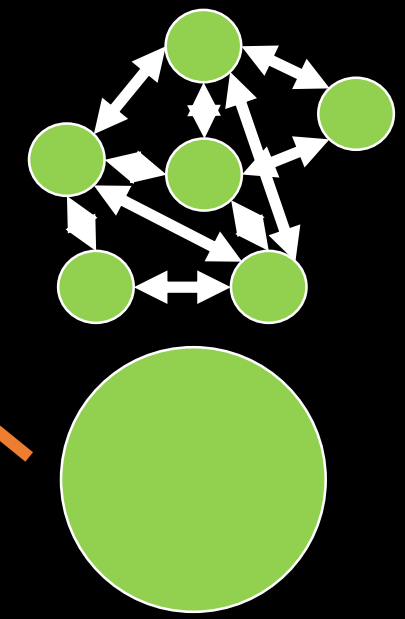
Inbreeding depression

spatial structure:
pollen dispersal $d_p = 1$

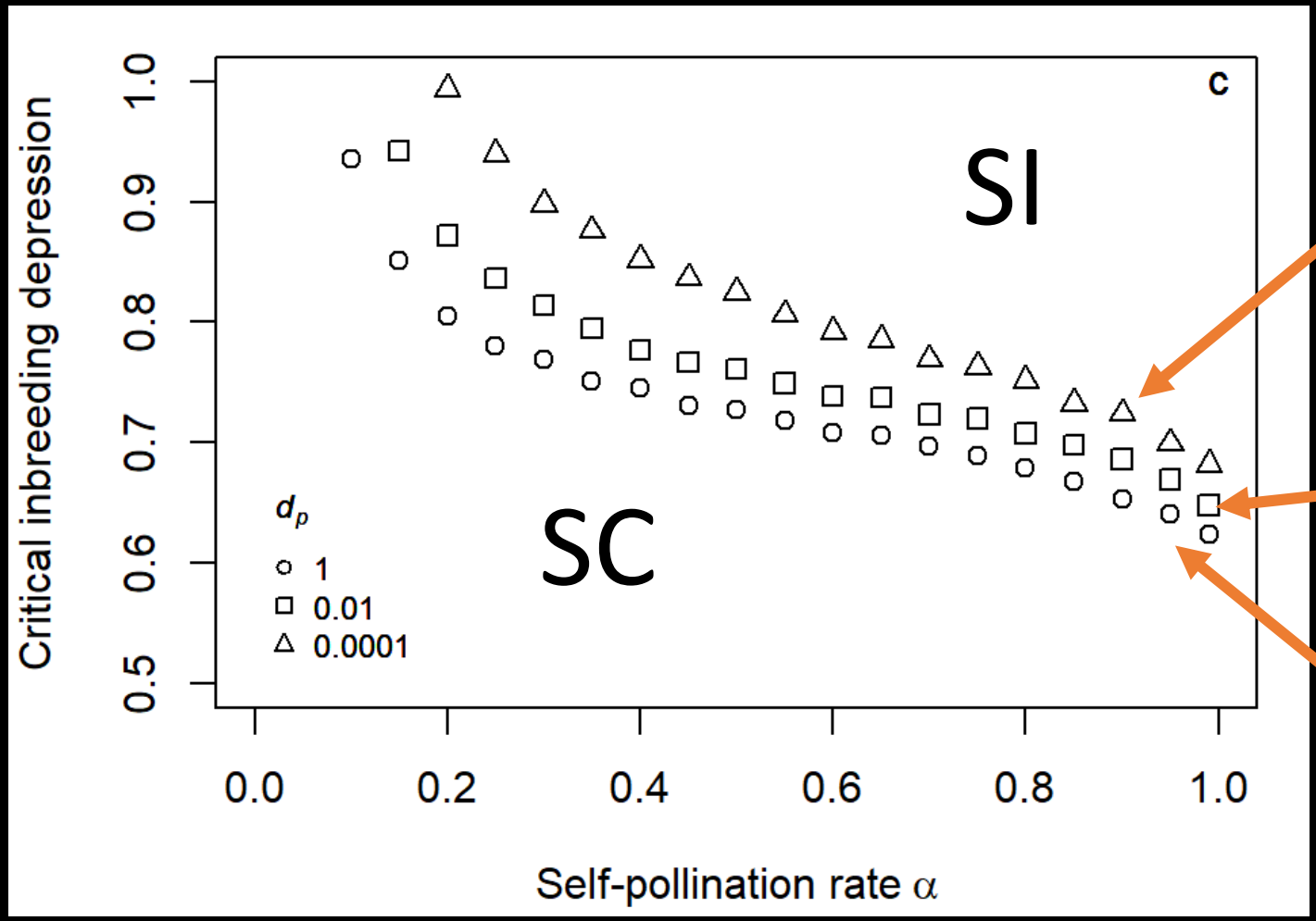


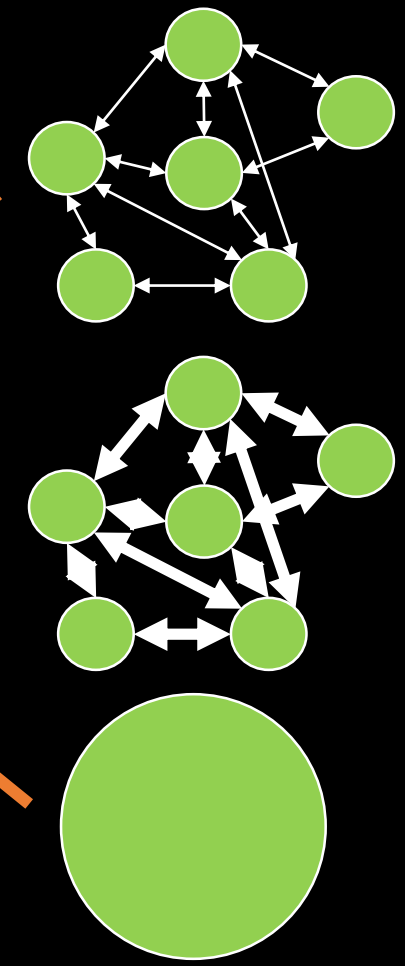
spatial structure:
pollen dispersal $d_p = 0.01$



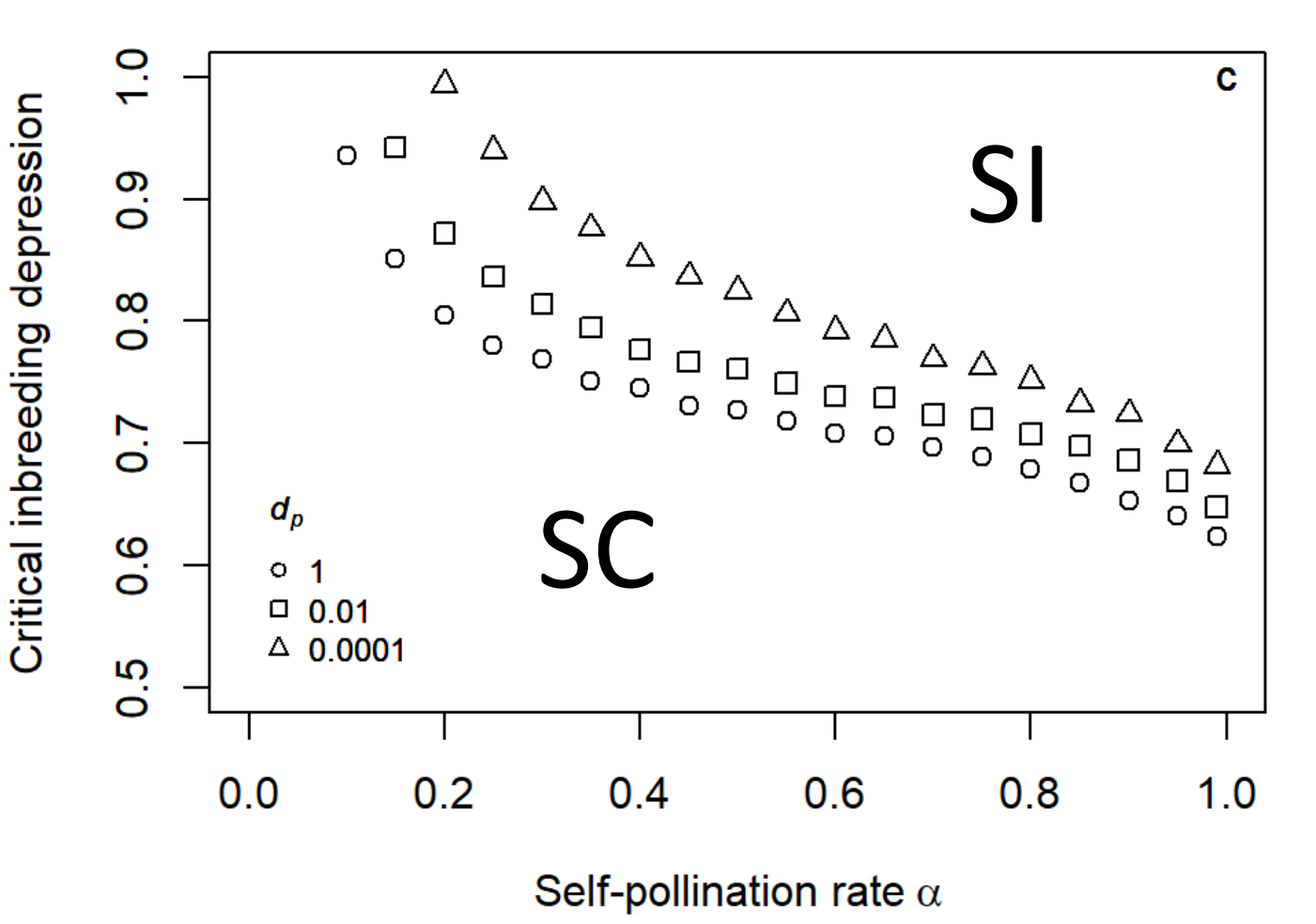


spatial structure:
pollen dispersal $d_p = 0.0001$





spatial structure: pollen dispersal rate

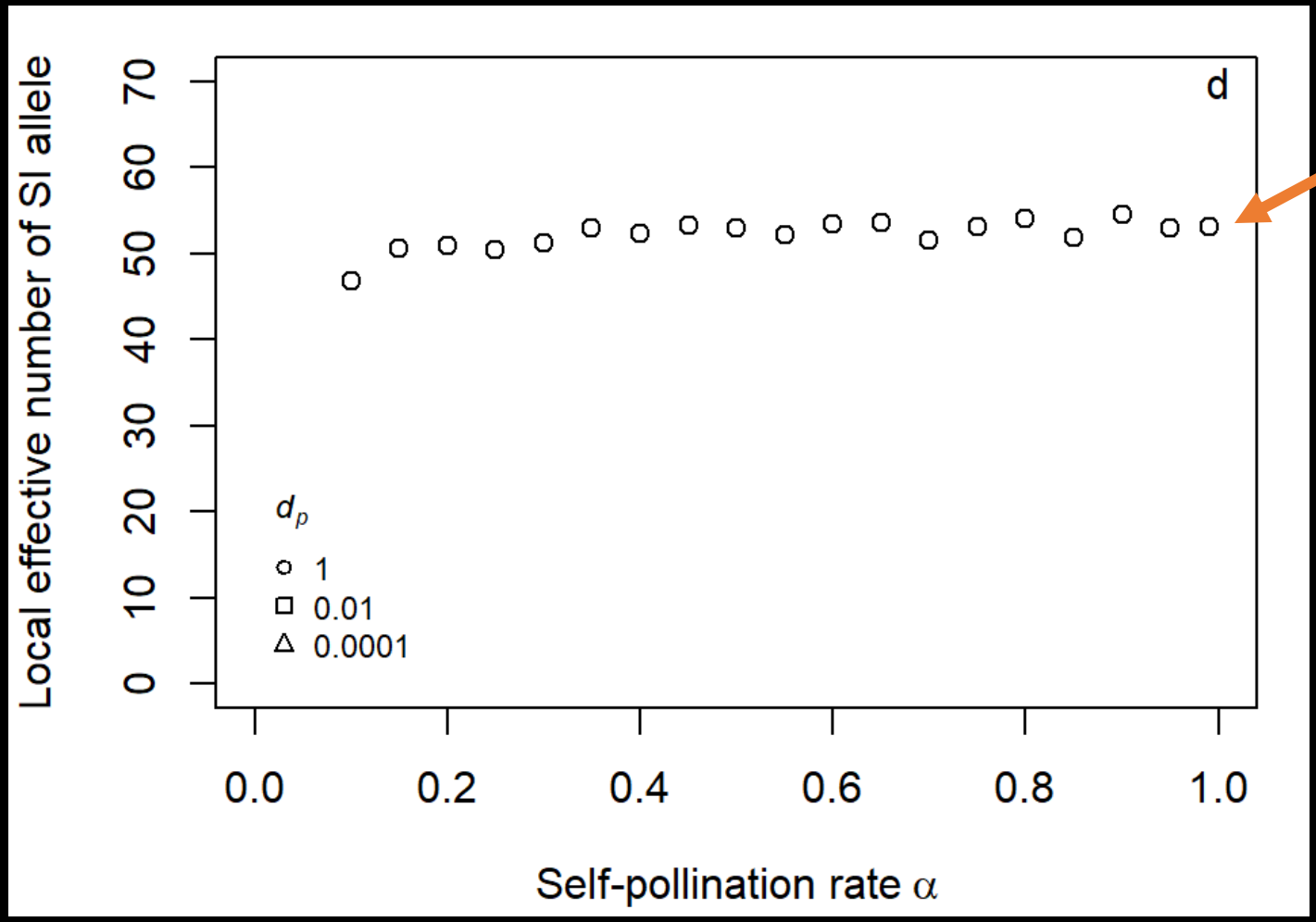


↘ pollen dispersal (d_p)

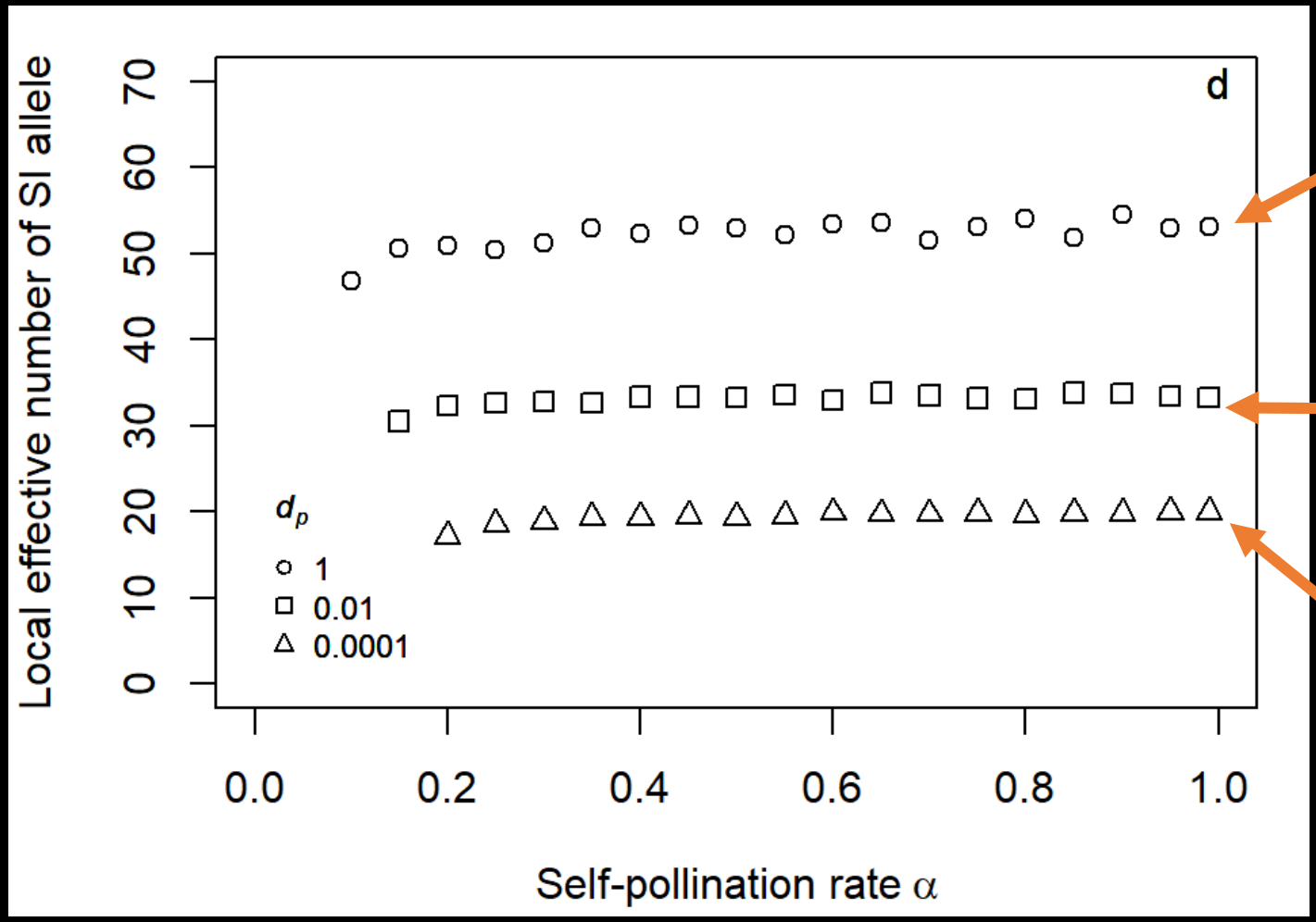
↗ critical inbreeding depression

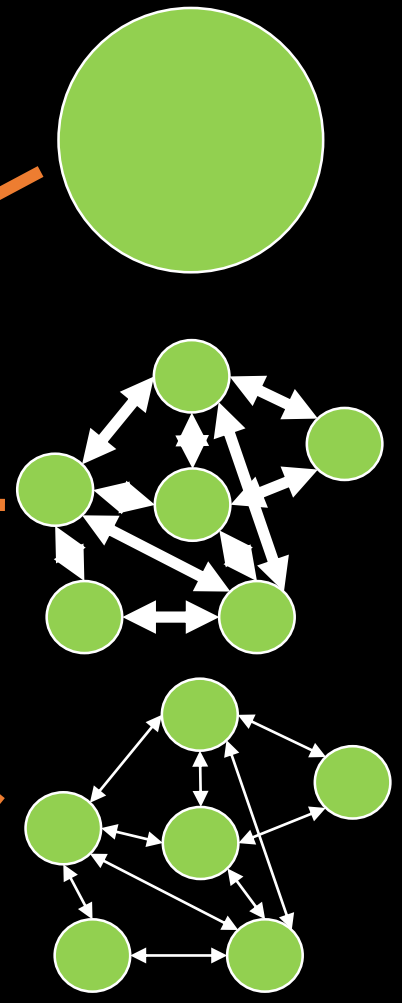
↘ resistance of the SI system

Local effective number of SI alleles

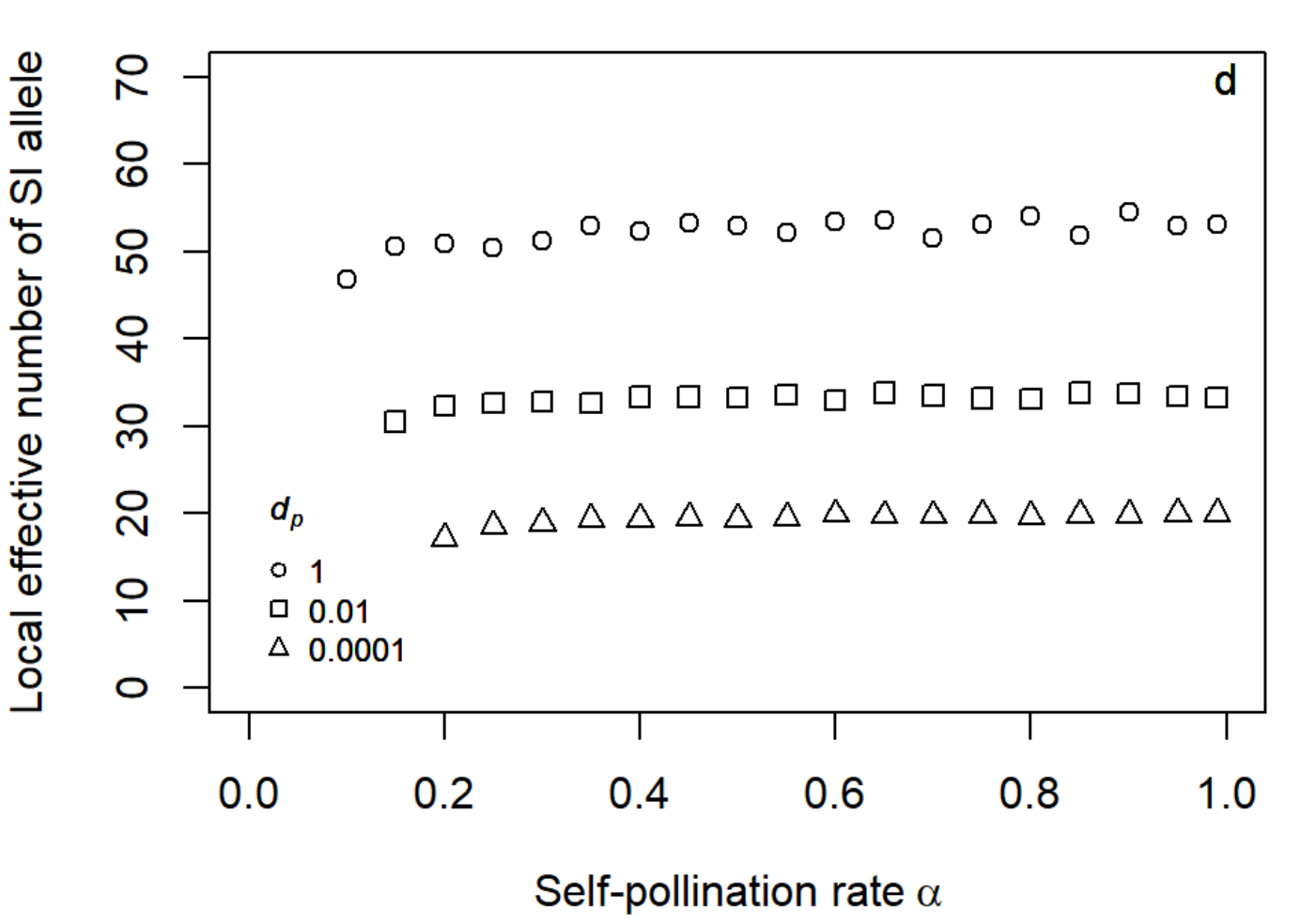


Local effective number of SI alleles





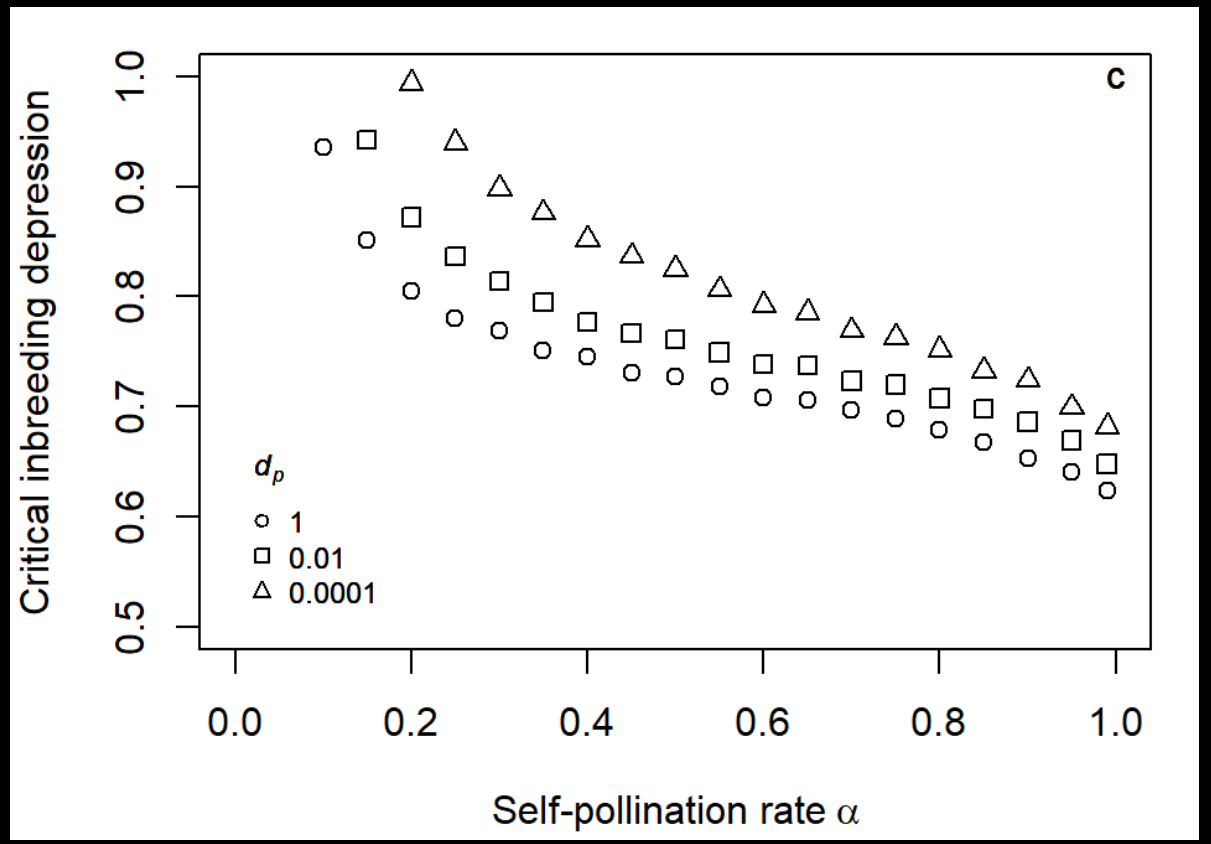
Local effective number of SI alleles

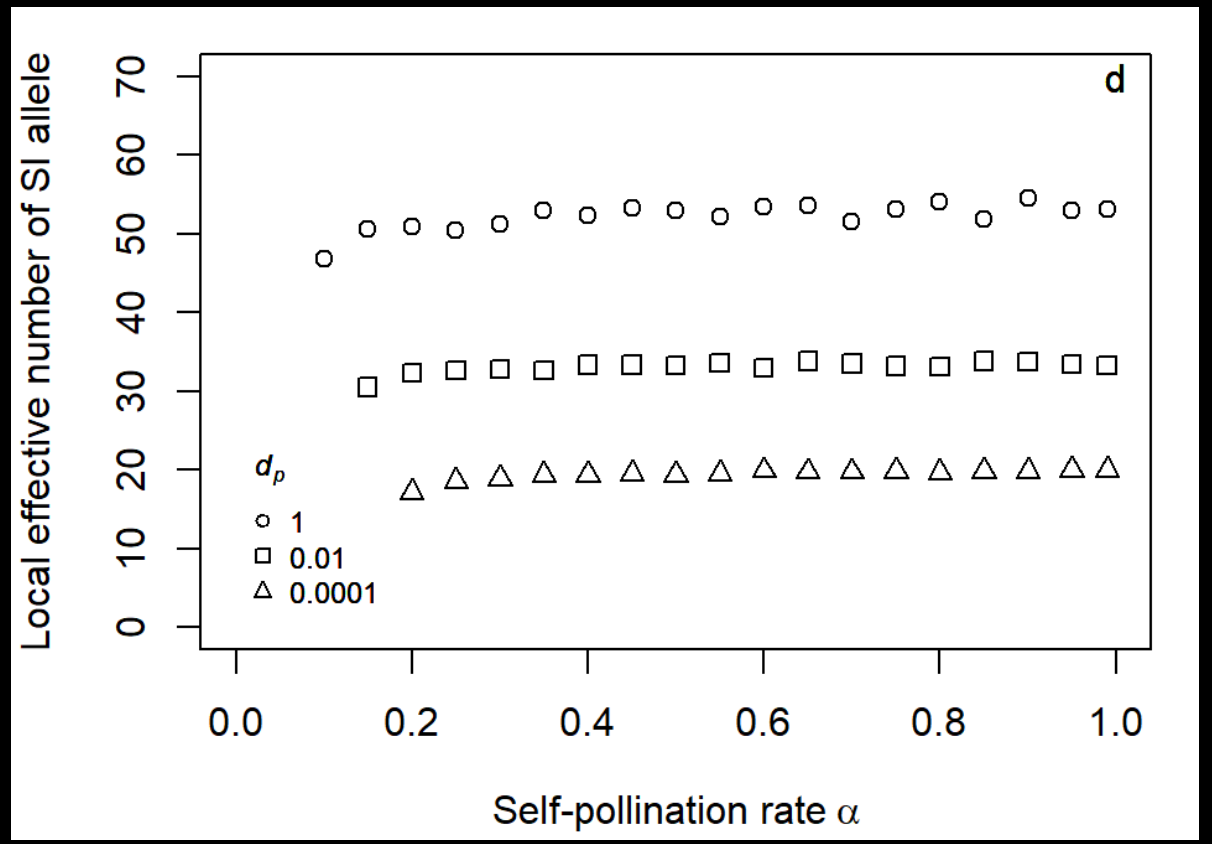


↘ pollen dispersal (d_p)

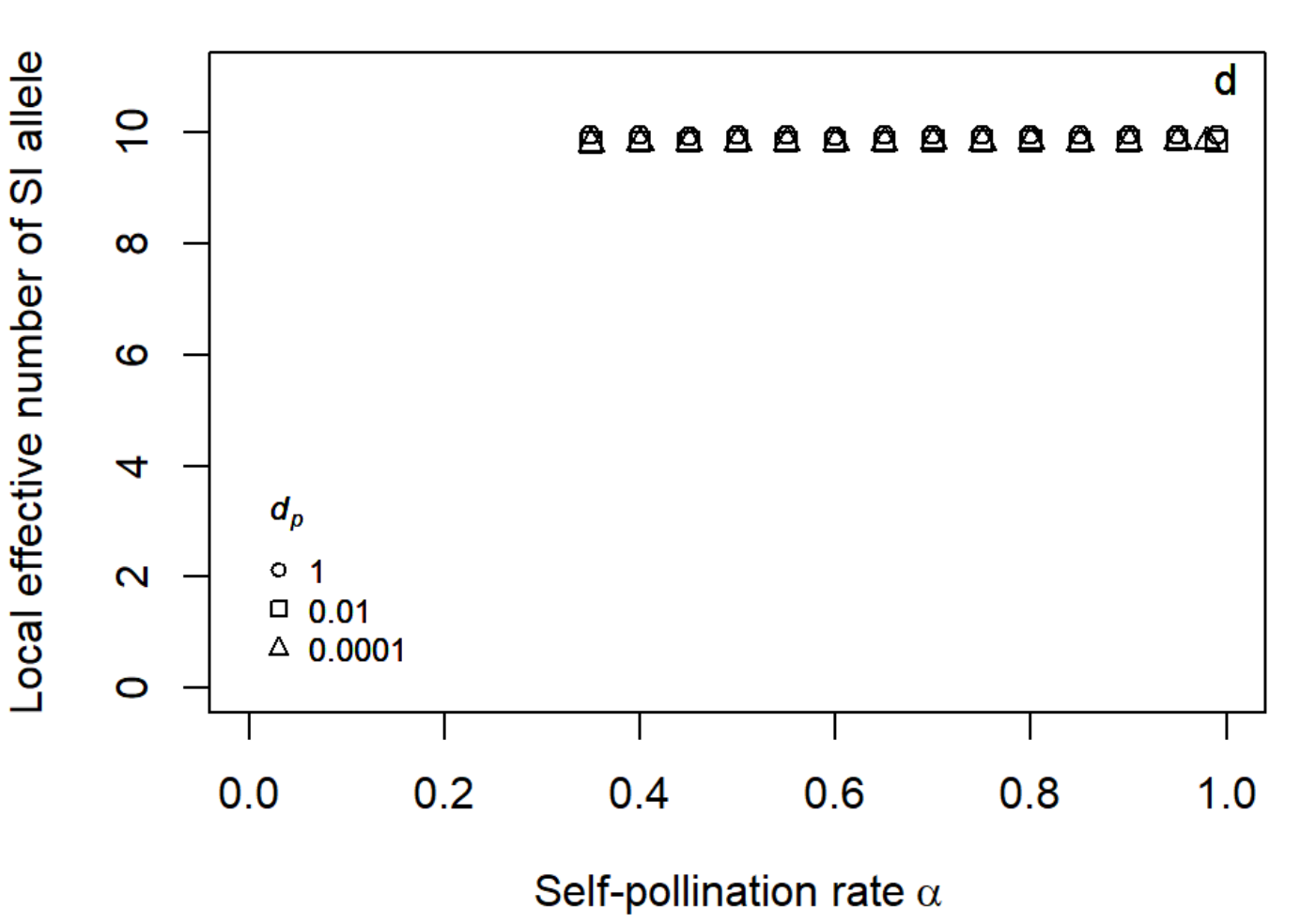
↘ local effective number of SI allele

Local effective number of SI alleles: correlation with system resistance



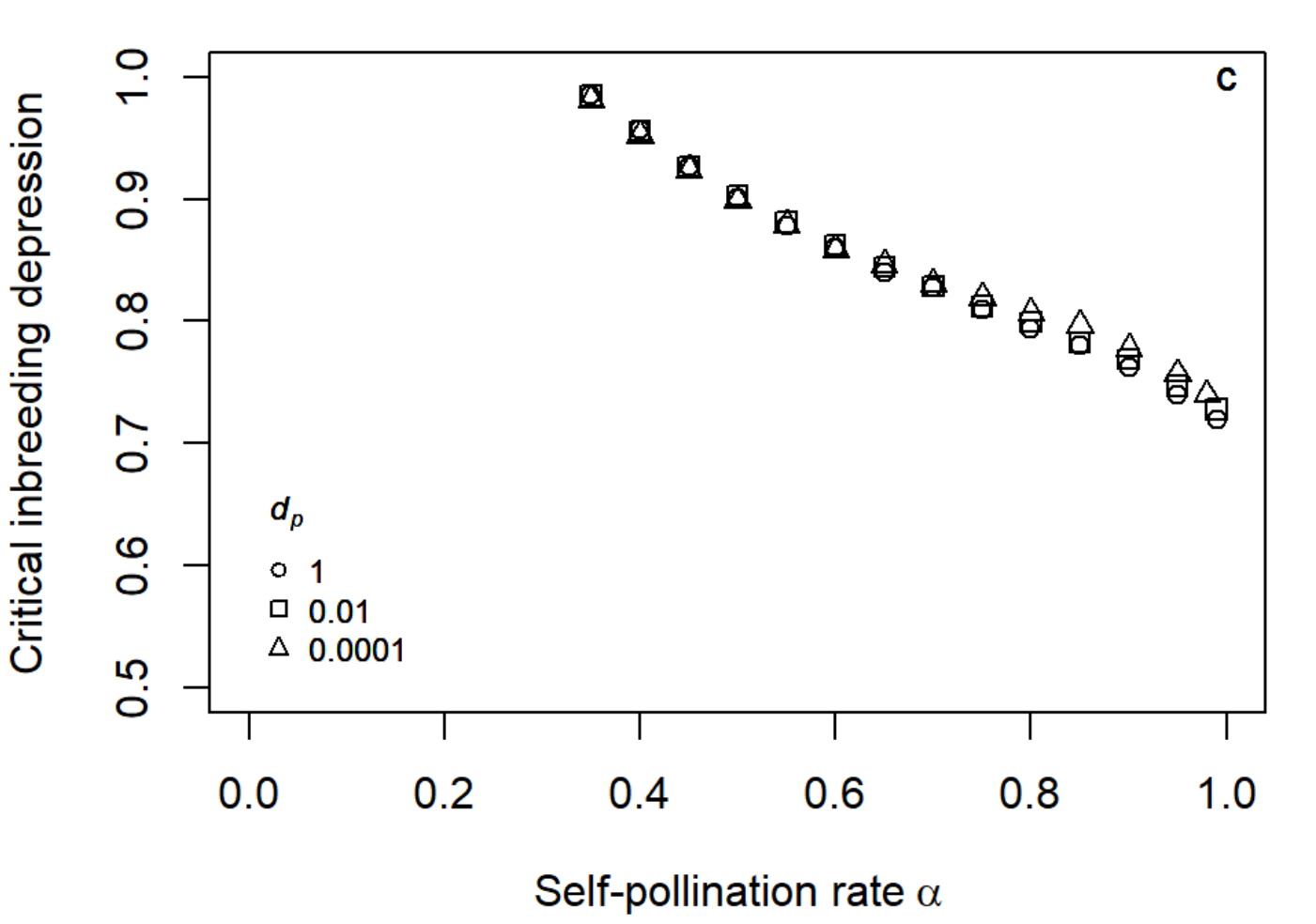


Local effective number of SI alleles: test with constant allele number



Artificially reduce SI allele number by reducing SI mutational space:
10 possible SI alleles

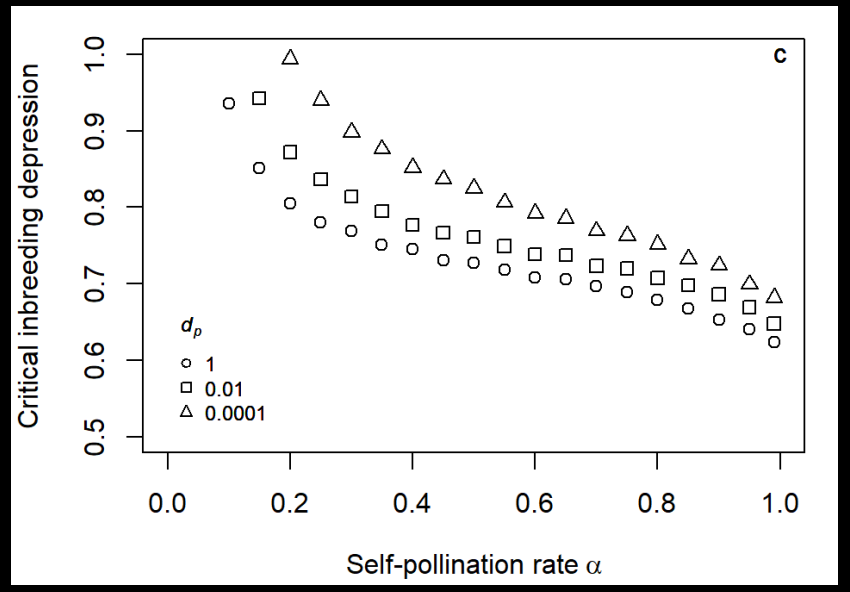
Local effective number of SI alleles: test with constant allele number

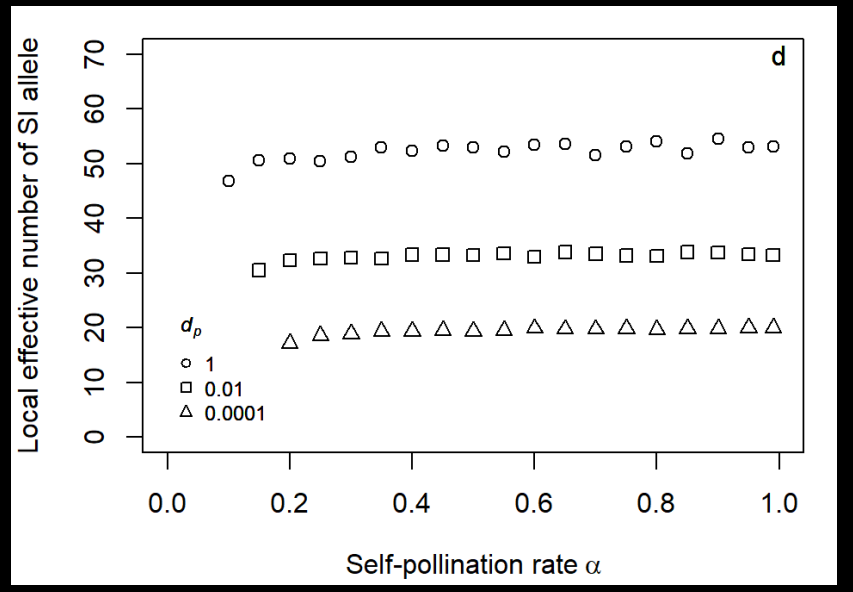


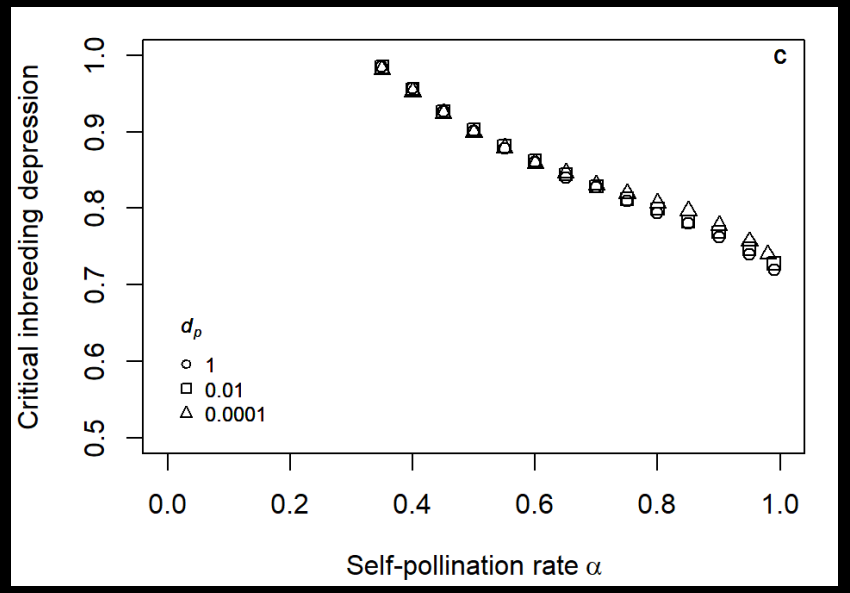
similar SI alleles number

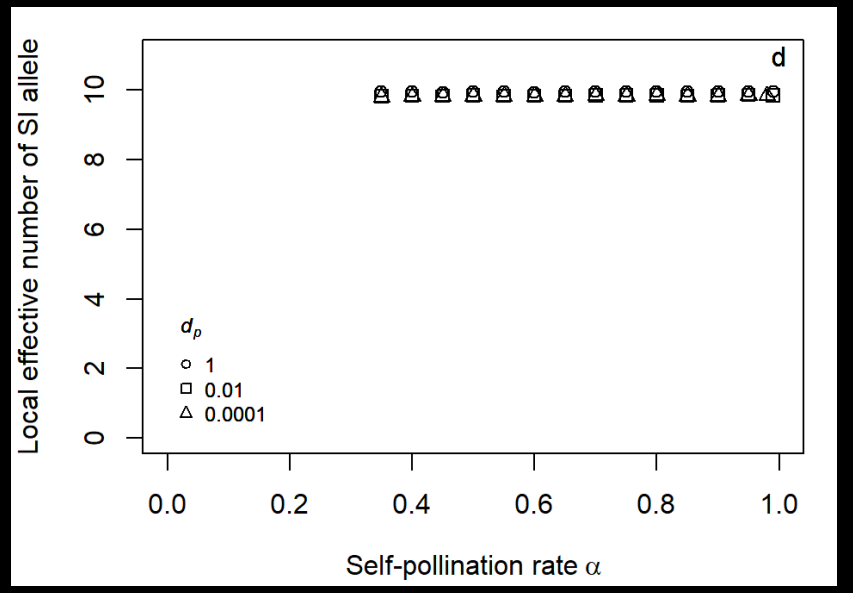
most of the effect of dispersal rate vanished

Local effective number of SI alleles



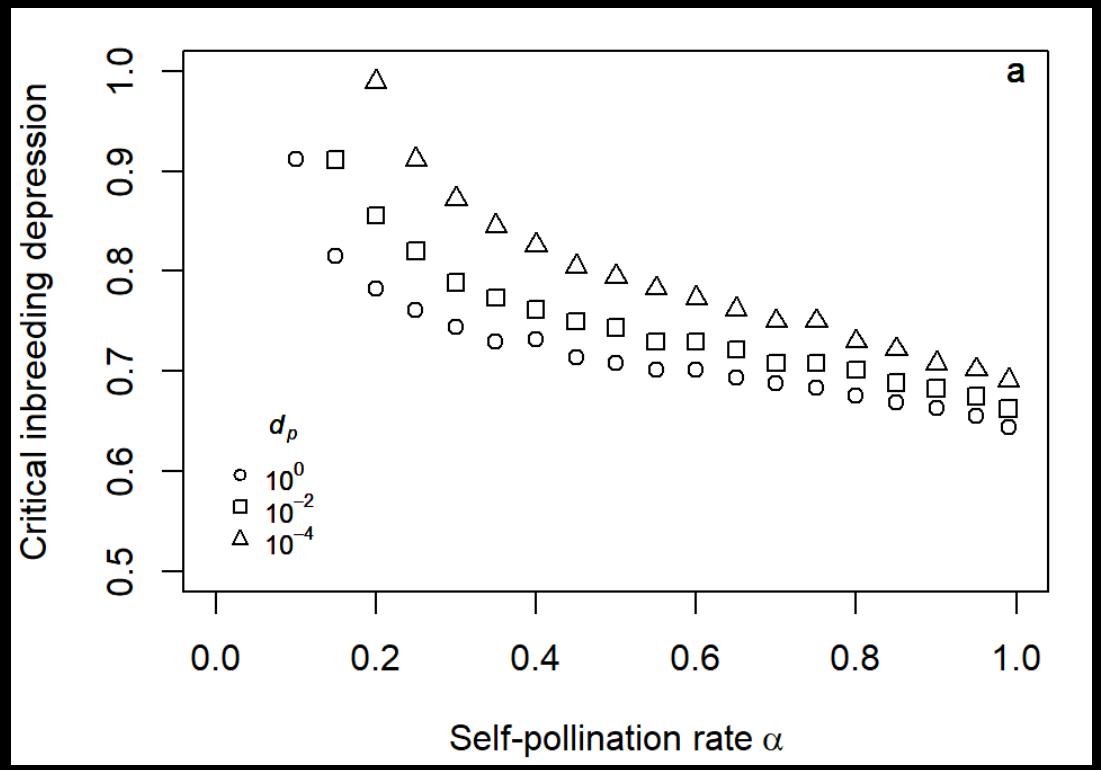




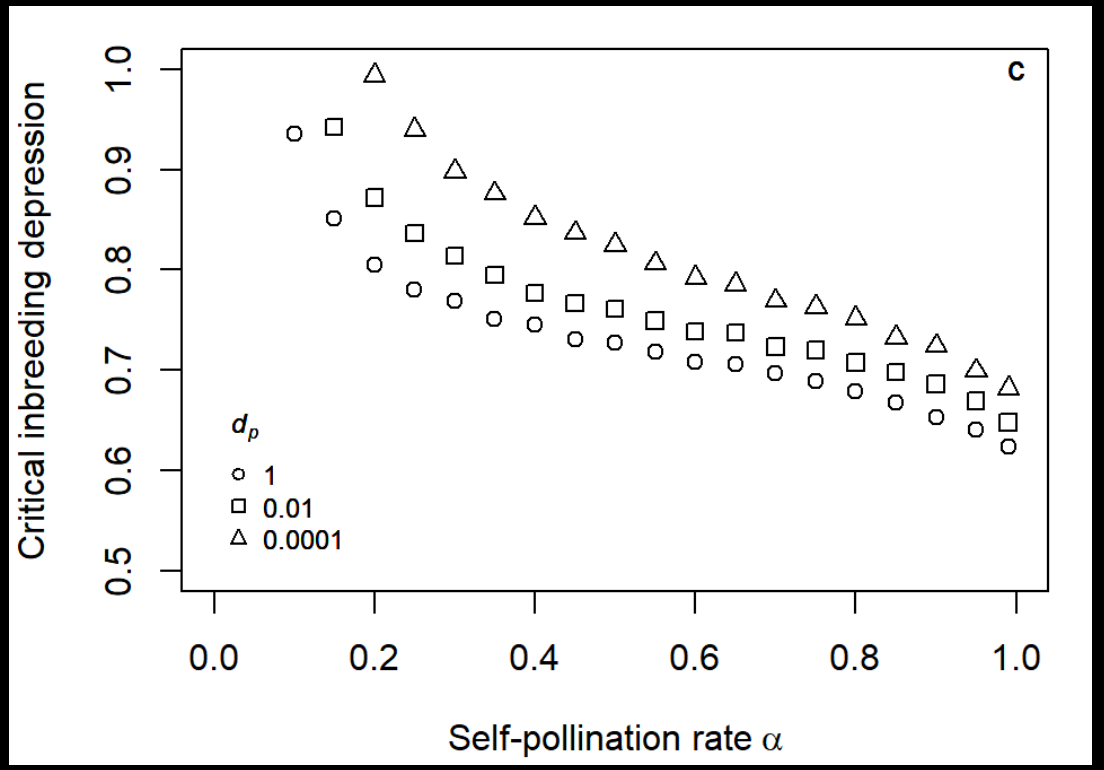


Inbreeding depression

δ constant

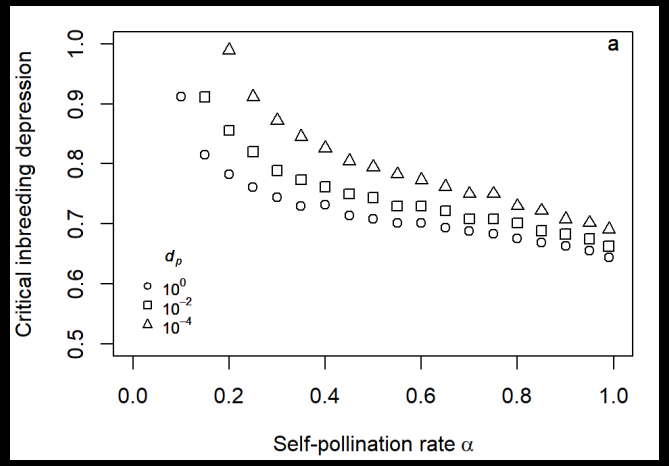


Explicit mutation model

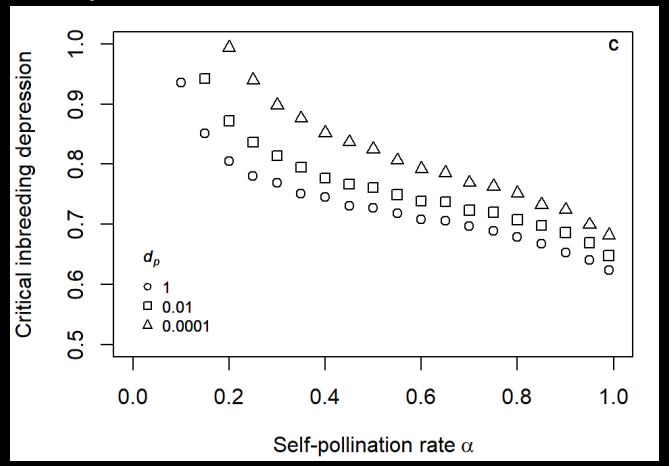


Inbreeding depression

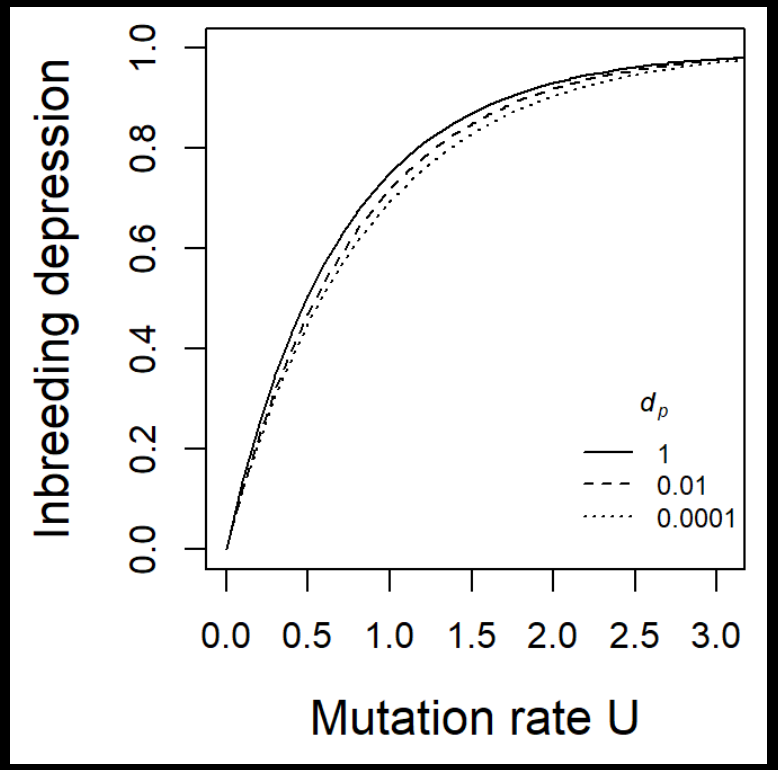
δ constant



Explicit mutation model



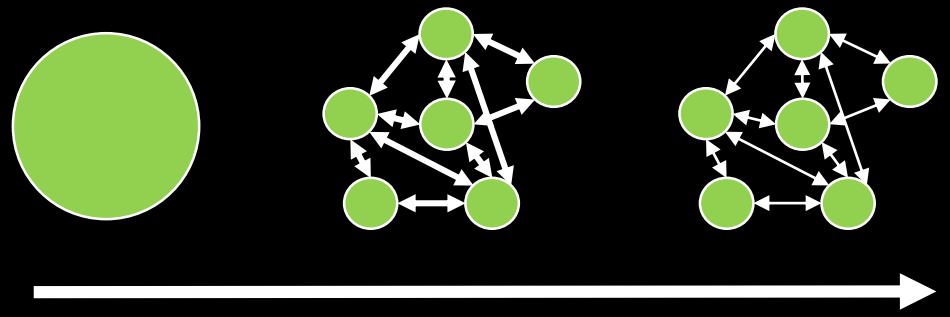
Explicit mutation model



Low effect of spatial structure on inbreeding depression

Explicit mutation modeling:
→ stochasticity
→ less SI allele
→ purging effect

Conclusion



spatial structure:

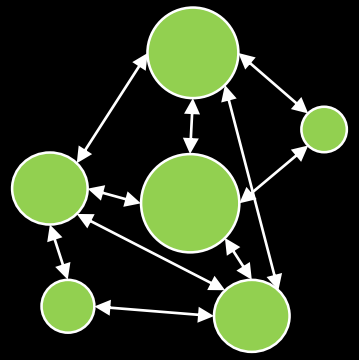
decrease SI system maintenance

main effect of the number of allele

small effect of spatial structure effects on inbreeding depression

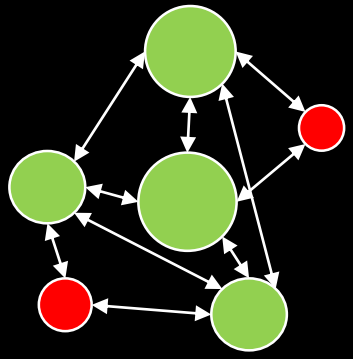
Perspective: different deme sizes

Different deme sizes → different number of alleles
→ different resistance to SC invasion.



Purging effect allow invasion of bigger deme ?

Mutation accumulation: SC extinction?



Thank you for your attention

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